

Transcriptomic, mutational and structural bioinformatics approaches to explore the therapeutic role of FAP in predominant cancer types

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Online Resource 3 Pan-cancer survival analysis using Kmplotter

Cancer	HR	p-value	High expression cohort	Low expression cohort
BLCA	1.58	0.008	28.63	106.1
BRCA	1.69	0.011	116.4	248.5
CESC	1.81	0.011	25.77	48.43
ESCA	1.81	0.136	24.33	59.37
HNSCC	1.61	0.0005	33.27	58.73
KIRC	1.62	0.001	74.23	118.47
KIRP	3.82	2.1e-06	21.93	86.97
LIHC	1.56	0.02	47.43	82.87
LUAD	1.36	0.05	45.97	55.1
LUSC	1.42	0.01	35.83	61.37
OV	1.27	0.07	41.97	48.2
PDAC	1.5	0.07	19.77	35.3
READ	0.59	0.18	47.73	36.53
SARC	0.82	0.38	28.33	29.9
STAD	1.69	0.001	20.23	56.2